

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 05:28:43 ; Search time 2658.23 Seconds

(Without alignments)
6925.982 Million cell updates/sec

Title: US-09-602-833A-1

Perfect score: 1116

Sequence: 1 atggagacataaagtgtgtt.....ctttagccttaacttga 1116

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues 2944280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBankl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_om:*

20: em_ov:*

21: em_or:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vl:*

30: em_htgo_hum:*

31: em_htgo_inv:*

32: em_htgo_rod:*

33: em_htg_hum:*

34: em_htg_inv:*

35: em_htg_rod:*

36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1116	100.0	1116	6 AX063232	AX063232 Sequence
2	1114.4	99.9	4860	9 HSA308569	AL308569 Homo sapi
3	683.2	61.2	172966	9 AC013467	AC013467 Homo sapi
4	681	61.0	681	6 AX063234	AX063234 Sequence
5	211.4	18.9	145795	2 HSA310996	AL310996 Homo sapi
6	211.4	18.9	202324	2 AC068720	AC068720 Homo sapi
7	161	14.4	202324	2 AC068720	AC068720 Homo sapi
8	130.4	11.7	2036	2 AK021919	AK021919 Homo sapi
9	80.2	7.2	150804	9 AC018500	AC018500 Homo sapi
10	80.2	7.2	164702	33 AC016333	AC016333 Homo sapi
11	80.2	7.2	166043	9 AC090947	AC090947 Homo sapi
12	80.2	7.2	185608	9 AC027126	AC027126 Homo sapi
13	67.2	6.0	216481	2 AC027653	AC027653 Mus muscu
14	64.4	5.8	169580	2 AC092762	AC092762 Pan trogl
15	63.6	5.7	1658	9 AF359380	AF359380 Homo sapi
16	63.6	5.7	2156	9 BC003193	BC003193 Homo sapi
17	63.6	5.7	2886	9 AF332199	AF332199 Homo sapi
18	63.6	5.7	165852	2 AC092874	AC092874 Sus scrofa
19	63.2	5.7	2754	2 BC003407	BC003407 Homo sapi
20	63.2	5.7	2846	9 BC008586	BC008586 Homo sapi
21	63.2	5.7	2847	9 AK022951	AK022951 Homo sapi
22	62.8	5.6	142296	2 AP004035	AP004035 Homo sapi
23	62.8	5.6	142396	9 HSAC000120	AL365337 Mus muscu
24	62.8	5.6	257967	2 AL365337	AL365337 Mus muscu
25	62.4	5.6	133841	2 AC079378	AC079378 Rattus no
26	62.4	5.6	188150	2 AC079378	AC079378 Rattus no
27	58	5.2	156294	2 AC092409	AC092409 Papio cyn
28	58	5.2	198746	2 AC092517	AC092517 Papio cyn
29	57.4	5.1	1127	9 AY007147	AY007147 Homo sapi
30	57.4	5.1	2384	6 AX099399	AX099399 Sequence
31	57.4	5.1	6409	9 AF263744	AF263744 Homo sapi
32	57.4	5.1	162598	2 AC079091	AC079091 Homo sapi
33	57.4	5.1	174297	2 AL512367	AL512367 Homo sapi
34	57.4	5.1	212127	2 AL391497	AL391497 Homo sapi
35	56.8	5.1	182366	2 AC041041	AC041041 Homo sapi
36	56.8	5.1	182885	2 AC087763	AC087763 Homo sapi
37	56.8	5.1	182914	2 AC090567	AC090567 Homo sapi
38	56.8	5.1	185510	2 AC011018	AC011018 Homo sapi
39	56.2	5.0	3214	3 CEL276590	AJ276590 Caenorhab
40	56.2	5.0	5109	10 RN066707	U66707 Rattus norv
41	55.8	5.0	2410	9 AK001332	AK001332 Homo sapi
42	55.8	5.0	5765	9 AB033051	AB033051 Homo sapi
43	55.2	4.9	3159	9 AB016816	AB016816 Homo sapi
44	55.2	4.9	6125	6 AX188327	AX188327 Sequence
45	54.2	4.9	5821	9 AF276423	AF276423 Homo sapi

ALIGNMENTS

RESULT	1	LOCUS	AX063232	1116 bp	DNA	PAT	24-JAN-2001
DEFINITION	Sequence 1 from Patent WO0078959.						
ACCESSION	AX063232						
VERSION	AX063232.1	GI:12541058					
KEYWORDS							
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
AUTHORS	Turner,A.C., Zambrowicz,B., Nehls,M., Friedrich,G.A. and Sands,A.T.						
TITLE	I (bases 1 to 1116)						
JOURNAL	Human genes and proteins encoded thereby						
FEATURES	Patent: WO 0078959-A 1 28-DEC-2000;						
source	Lexicon Genetics Incorporated (US)						
	Location/Qualifiers						
	1..1116						
	/organism="Homo sapiens"						
	/db_xref="taxon:9606"						

CDS

1. 1116
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC35077.1"
/db_xref="GI:12541059"
/translation="MGKRVVFEIDSVIRALMETRVKKHKAOKKEVERLEKSALEKIK
EEMNFVACRRKGIPOAVYCKNGFIDTSVRLDDIENNTLIOTIOLFOEMRIIDLPKDRSSAV
FELSGEHMTELPDSLKQOTHLREWIISNTLIOTIOLFOEMRIIDLPKDRSSAV
AEICGLNKEANFYNIKSIPELDCEGLERDGSNTELMELPEPESLNKOYF
VDISANKSESPICVLMSNOMIDISSNNITLPODIRLEILOSFLTKNKLTYLP
XSMNLKKTLIVYSGDHVLELPALDSSIPKLFYSLMDNPIDNACEDGNEIMESB
RDRHDEKWEKATIEDLKEREVSPTTKVFSQL"

BASE COUNT 343 a 224 c 265 g 284 t

ORIGIN

Query Match 100.0%; Score 1116; DB 6; Length 1116;
Best Local Similarity 100.0%; Pred. No. 9.2e-283;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggagacataaagtgtgtcttcgcacacattctgcacacagacctgtggaacctgt 60
DB 1 ATGGAGACTAAAGTGTGTCTCTGCACATTTCTGCATCAGAGCCTTGTGGAAACTG 60

QY 61 gtcaagaagcaaaagcttggcagaagaagaaggttgaaggcttgagaagaagcgcttg 120
DB 61 GTCAAGAAGCAAAAGCTTGGCGAGAGAAGAGGTGGAAGAGCTTGAGAAGAGCCCTTG 120

QY 121 gagaagaataaaggagagatgtgaacttctgtgcccgaatgcagaagaagaaggacatcccccag 180
DB 121 GAGAAGATAAAGGAGAGATGTGACTTTGTGGCCGAATGCAGAGAGAGGATCCCCCAG 180

QY 181 gctgtatactgcaagaatgtgtctatagacacacagcgtgcgcttcgtgaacaattgaa 240
DB 181 GCTGTATACTCAAGAAATGCTTCATATAGACACACAGCTGCGCTTGTGACAAATGAA 240

QY 241 aggaacaccttcacaagacagagttcacttcccaagacagagaggaacagagcgagtcg 300
DB 241 AGGAACACTCTCACAAAGCAGAGTTCACTCCCAAGACAGAGGCAAAAGCGAGCTG 300

QY 301 ttctgttctgaccttctcgggagacagcgtgcgagcctccagattcattgaagaagcag 360
DB 301 TTTGTGTTTGAACCTTCTCGGGAGACAGCTGCAGAGCTCCAGATTCTTGAAGAGCAG 360

QY 361 acacacctgagagaatgtgtacataaagcaatccttgattcaaatcattcctacatat 420
DB 361 ACACACCTGAGAGAATGTGTACATAAGCAATCCTGTGATTCAATCATCTCATATAT 420

QY 421 cagttattcaagcagatagaattctgtatctgcacaaaaaaccacaaattcacaatttca 480
DB 421 CAGTTATTCAAGCGATAGAAATCTGGATCTGCCAAAAAACCAAAATCTCACATCTTCA 480

QY 481 gcagaataatcggttctttaaagaacctgaagaactcaatgttggtttcaactatctgaag 540
DB 481 GCAGAATAATCGGTTGTTTAAAGAACTGAAAGAACTCATGTGGTTTCACTATCTGAAG 540

QY 541 agcattccctcagaatgtggagatgtgaaaaatctagagagacttgattgttcggaat 600
DB 541 AGCATTCCTCCAGAAATGGAGATGTGAAAAATCTAGAGAGAGCTGATTGTCTGGAAT 600

QY 601 ctgaataatgaagcgtgccttcttgaaatgaatgaatgaagaagctgtacatttgtagat 660
DB 601 CTGAATAATGAAGCGTCCCTTCTGAATTAATTAATTTGAAGCAAGTTACATTTTGAAT 660

QY 661 atctcagaacaagaattctcagtgctccaatctgtgctcgcgagatgtcgaaattgcaag 720
DB 661 ATCTCAGCAAAAGACTTTTCCAGTGTCCCATCTGTCTCTCGGATGTCCGAATTTGCAG 720

QY 721 tggttgatatcagcagcaataaactgcagacctgcgcgaagatatagacagcgctagag 780
DB 721 TGGTTGATATCAGCAGCAATAAAGCTGACGACCTGCCGCAAGATATAGACAGCGCTAG 780

QY 781 gagctgcagagcttctctgttataaaaaaagaattgacctcctcctattcactgctg 840

DB 781 GAGCTGCAGAGACTTCTCTGTATAAAAACAAGTTGACCTACCTCCATTCATGCTG 840

QY 841 aacccgaagaagctcactctgtatgtcagtcagtcggagaccatttgtagactcccaact 900
DB 841 AACCGAAGAAGCTCAGTCTGTATGCGTCAAGTGGGACCATTTGTGGAGCTCCCAACT 900

QY 901 gcccttctgactcaccacacaccttaaatctgaaacccctatggaacatcctatgat 960
DB 901 GCCCTTGTGACTCATTCACACCTTTAAATTTGAAGCCTTATGACATCTTATGAT 960

QY 961 aatgcccaatgtgaagatgtgcaatgaataatgaagaagtgaagcgagatcgccaacttt 1020
DB 961 AATGCCCAATGTGAAGAGGCGCAATGAATATGAAGAAAGTGAACGGATCGCCACATTTT 1020

QY 1021 gataaagaagtataaagccctatatatgaagaccttaagaagaagaagaatctgtccagc 1080
DB 1021 GATAAGAAGTATATAAGCCTATATTTGAAGACCTTTAAGAAAGAAATCTGTCCAGC 1080

QY 1081 tataccaccaagtgctctttagccttcaacttga 1116
DB 1081 TATACCACCAAGTGTCTTTAGCTTCAACTTGA 1116

RESULT 2
HSA308569
LOCUS
DEFINITION
HSA308569 4860 bp mRNA PRI 06-JUN-2001
Homo sapiens mRNA for leucine-rich repeat-containing 2 protein (LRRC2 gene).
AJ308569
VERSION
AJ308569.2 GI:14330408
KEYWORDS
leucine-rich repeat-containing 2 protein; LRRC2 gene.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 4860)
Kiss, H., Yang, Y., Kost-Alimova, M., Szeles, A., Kholodnyuk, I., Kedra, D., Kiss, C., Klein, G., Imreh, S., and Dumanski, J. P.
Transcriptional map of the Common Eliminated Region 1 on human 3p21.3
Unpublished
2 (bases 1 to 4860)
Kiss, H.
REFERENCE
Direct Submission
Submitted (27-FEB-2001) Kiss H., Microbiology and Tumorigenology Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177, SWEDEN
REMARK
Revised by [3]
3 (bases 1 to 4860)
Kiss, H.
REFERENCE
Direct Submission
Submitted (06-JUN-2001) Kiss H., Microbiology and Tumorigenology Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177, SWEDEN
COMMENT
On Jun 8, 2001 this sequence version replaced gi:13186111.
FEATURES
source
1. 4860
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21.3"
168. 1283
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168. 1283
/gene="LRRC2"
/gene="LRRC2"
/codon_start=1
/product="leucine-rich repeat-containing 2 protein"
/protein_id="CAC33442.1"
/db_xref="GI:13186112"
/translation="MGKRVVFEIDSVIRALMETRVKKHKAOKKEVERLEKSALEKIK
EEMNFVACRRKGIPOAVYCKNGFIDTSVRLDDIENNTLIOTIOLFOEMRIIDLPKDRSSAV
FELSGEHMTELPDSLKQOTHLREWIISNTLIOTIOLFOEMRIIDLPKDRSSAV

AEIGCLKNIKELNVGNFYKLSIPPELGDENLERLDCSGNLELMELEPFELSNKQVTF
 VDISANKFSSVPICTJLWMLDISNMLJLPODIDLEJESFLKXNKLUTYLP
 YSMLNKLITLIVVSGDLVELPDLJLDSSTPLKFPVSLMDNPNIDNOCEDGNLMESE
 RDRQHEDEKEMKRYIEDLKERESVPSYTTIVSRSLQ"

BASE COUNT 1480 a 924 c 1162 g 1294 t
 ORIGIN

Query Match 99.9% Score 1114.4; DB 9; Length 4860;
 Best Local Similarity 99.9%; Pred. No. 3.1e-282;
 Matches 1115; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atggagacataaagtgtgtgtcttcgacattctgtcatcagagccttgggaaactcgt 60
 DB 168 ATGGACATTAAGTGTGTGCTTGTGACATTTCTGTCAAGAGCCTTGTGGAAACGCT 227
 QY 61 gtcaagaagacaaagcttggcagaagaagggtgaaagcttgaaagcgccttg 120
 DB 228 GTCAAGAGACCAAAAGCTTGGCAGAGAGAGAGGCTTGAAGAGCGCCTTG 287
 QY 121 gagaagaataaggaggtgtggaacttggccgaatgcagaggaagggatcccccag 180
 DB 288 GAGAGATTAAGAGGAGGTGTGTGCTTGTGCAAGAGAGAGAGGAGGAGGAGGAGGAGG 347
 QY 181 gctgtactcagaagatggtctcatagacacagcgtgcggtcttcgcaagaattgaa 240
 DB 348 GCTGTATCTGCAAGAAATGGCTTCAATAGACACAGCGCTTCTTGACAGATTTGAA 407
 QY 241 aggaacacatcacaagcagagttcattcccaagaagcagaagcagaagcagtcg 300
 DB 408 AGGAACACTCTCAACAGCAGAGATTCTCCCAAGAGACAGAGCAACGAGCAGTGGC 467
 QY 301 tttgtgttgaactttctgggggagcacttgcagcagcgtcccaagattatgaagagcag 360
 DB 468 TTTGTGTTTAACCTTTCTGGGAGCACTGAGCGAGCTCCAGATTATTTGAAGAGCAG 527
 QY 361 acacacactgagagaatgtatcataagaacaacttgaatccaacttccatatactat 420
 DB 528 ACACACTGAGAGATGTGATAGCAATACCTTGATTCAAATCATCTCTACTATATTT 587
 QY 421 cagttattcaagcagatgagaaattcggatctgcacaaacacaaatccaactcca 480
 DB 588 CAGTTATTTCAAGAGATGAGAAATTTCTGATCTGCCAAAAAACCAATCTCAATCTTCCA 647
 QY 481 gcggaatcggtgtgttgaagaacctbgaagaactcaatgtgttcaactatcgaag 540
 DB 648 GCGAATAATCGGTGTGTGAAGAACCTGAAGAACTCATGTGGTTCACTATCTGAAG 707
 QY 541 agaatctccagaatgtgagatgtgaaatcttagagaagcgtgattcttcgaaat 600
 DB 708 AGCAATCTCCAGAAATGGAGATGTGAAATCTAGAGAGCTGAGATTTGTTCTGGAAT 767
 QY 601 ctagaatlaatgagctgaccttgaattgaattgaagcaagttacattgtatag 660
 DB 768 CTAGAATTAATGAGAGCTGCCCTTTGAATTAATTAATTTGAAGCAAGTTACATTTGTAGAT 827
 QY 661 atctcagcaacaagtttccagtgctcccaatcgtgtcctcgtgagatgtcgaat 720
 DB 828 ATCTCAGCAACAAGTTTCCAGTGCTCCCAATCTGTGTCTGCGAGTGTGAATTTTCAG 887
 QY 721 tggctgatactcagcaacaaactcagcagccttcgcaagaatataagaagcgtgag 780
 DB 888 TGGTGTGATATCAGAGCAATTAACCTGACGACCTGCCGCAAGATATAGACAGCTTAGAG 947
 QY 781 gagctcagagcttctctgtataaaacaagttgacctacattccctatccatgctg 840
 DB 948 GAGCTGAGAGCTTCTCTGTATAAAAACAAGTTGACCTTACCTTCCCTATTTCCATCTG 1007
 QY 841 aaactaagaagcctcactcgttagtgcgtgaggaacatttggggagcctcccaact 900
 DB 1008 AACCTGAGAGAGCTCACTCTGTTAGTGTGAGTGGAGCAATTTGGTGGAGCTCCCACT 1067
 QY 901 gcccttgtgactcatccacactttaaaattgttaagccttataygacaactccatgat 960

DB 1068 GCCCTTGTGACTCATCCACACCTTTAAATTTGTAAGCCTTATGAGCAATCTATGAT 1127
 QY 961 aatgcccaatgtgaagatgagcaatgaataatgaaagtgaaagtgagcagccatctt 1020
 DB 1128 AATGCCCAATGTGAAGTGGCAATGAATAATATGAAAGTGAACGAGGAGTCCCAACTTTT 1187
 QY 1021 gataagaagtatgaagaagcctatataatgaagccttaagaagaagaatcgttccagc 1080
 DB 1188 GATTAAGAGATTATGAAGCCTTATATTTGAAAGCCTTTAAAGAAAGAGATCTGTTCCAGC 1247
 QY 1081 tataccaacaagtgctctttagccttcaatttga 1116
 DB 1248 TATACCAACCAAGTGTCTTTAGCCTTCAACTTTGA 1283

RESULT 3
 AC013467/c
 LOCUS AC013467 172966 bp DNA PRI 25-MAY-2001
 DEFINITION Homo sapiens clone RP11-451F14, complete sequence.
 ACCESSION AC013467
 VERSION AC013467.8 GI:14196420
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 172966)
 WATERSTON, R.H.
 TITLE The sequence of Homo sapiens clone
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 172966)
 WATERSTON, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (12-NOV-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

REFERENCE 3 (bases 1 to 172966)
 WATERSTON, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAY-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA

COMMENT Center project name: H_NH0451F14.
 On May 25, 2001 this sequence version replaced gi:13624417.

FEATURES
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 Location/Qualifiers
 1..172966
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="RP11-451F14"

BASE COUNT 57371 a 34327 c 31782 g 49486 t
 ORIGIN

Query Match 61.2% Score 683.2; DB 9; Length 172966;
 Best Local Similarity 86.2%; Pred. No. 1.4e-168;
 Matches 828; Conservative 0; Mismatches 118; Indels 14; Gaps 6;

QY 1 atggagacataaagtgtgtgtcttcgacattctgtcatcagagccttgggaaactcgt 60
 DB 169367 ATGGATATCAAAAGTGCATATTGACATTTCTGTGTCAGAGCCTTGTGGAAACCTGT 169308
 QY 61 gtcaagaagacaaagcttggcagaagaagggtgaaagcttgaaagcgccttg 120
 DB 169307 GTCAAGAGACAC -AAGTTTGGCAGAAAGAGGAGCAAAAGTCTTGAGAAAGTGCATCA 169249
 QY 121 gagaagaataaggaggtgtggaacttggccgaatgcagaggaagggatcccccag 180
 DB 169248 GAAAGAGCAAAAGAGAGAGTGGCCCTTGAGAGTCAAGTGCAGAGAGAAAGCATCTCTCG 169189
 QY 181 gctgtata---ctgcaagaatggtctcatagaca---caagcgtgcgcttctgacaa 233
 DB 169188 GCTGAGTACTGCTGGGATAGTGTGCTTCAATAGACATTCATAGCATGCAAGCTTGTGAAAA 169129

[illegible]

ORGANISM Homo sapiens
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
 Mammalia: Eutheria: Primates: Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 145795)
 AUTHORS Kiss, H., Yang, Y., Kost-Alimova, M., Szekes, A., Kholodnyuk, I.,
 Kedra, D., Kiss, C., Klein, G., Imreh, S., and Dumnanski, J. P.
 TITLE Transcriptional map of the common eliminated region 1 on human
 3p21.3
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 145795)
 AUTHORS Kiss, H.
 TITLE Direct Submission
 JOURNAL Submitted (17-APR-2001) Kiss, H., Microbiology and Tumorbiology
 Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
 SWEDEN
 COMMENT The sequencing contigs are in order and the gaps between them are
 represented by 100 n's.
 Contig 1: 1-2508 Contig 2: 2609-17434 Contig 3: 17535-21987
 Contig 4: 22088-23066 Contig 5: 23167-28845
 Contig 6: 28946-30840 Contig 7: 30941-37879 Contig 8:
 37980-38928 Contig 9: 39029-40834 Contig 10: 40835-44527 Contig
 11: 44628-48077 Contig 12: 48178-52755 Contig 13: 52856-53293
 Contig 14: 53394-54768 Contig 15: 54869-57895 Contig 16:
 57996-59322 Contig 17: 59423-60159 Contig 18: 60260-61231
 Contig 19: 61332-62928 Contig 20: 63029-63852 Contig 21:
 63953-75555 Contig 22: 75656-77760 Contig 23: 77861-79686
 Contig 24: 79787-80857 Contig 25: 80958-87622 Contig 26:
 87723-89164 Contig 27: 89265-90007 Contig 28: 90108-92035
 Contig 29: 92136-97298 Contig 30: 97399-102032 Contig 31:
 102133-106605 Contig 32: 106706-108263 Contig 33: 108364-110022
 Contig 34: 110123-113747 Contig 35: 113848-125151 Contig 36:
 125252-126026 Contig 37: 126127-129649 Contig 38: 129750-132160
 Contig 39: 132261-133125 Contig 40: 133226-135661 Contig 41:
 135762-142148 Contig 42: 142249-145795.
 * NOTE: This is a working draft sequence. It currently
 * consists of 42 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 2508: contig of 2508 bp in length
 * 2509 2608: gap of 100 bp
 * 2609 17434: contig of 14826 bp in length
 * 17435 17534: gap of 100 bp
 * 17535 21987: contig of 4453 bp in length
 * 21988 22087: gap of 100 bp
 * 22088 23066: contig of 979 bp in length
 * 23067 23166: gap of 100 bp
 * 23167 28845: contig of 5679 bp in length
 * 28846 28945: gap of 100 bp
 * 28946 30840: contig of 1895 bp in length
 * 30841 30940: gap of 100 bp
 * 30941 37879: contig of 6939 bp in length
 * 37880 37979: gap of 100 bp
 * 37980 38928: contig of 949 bp in length
 * 38929 39028: gap of 100 bp
 * 39029 40834: contig of 1806 bp in length
 * 40835 40934: gap of 100 bp
 * 40935 44527: contig of 3593 bp in length
 * 44528 44627: gap of 100 bp
 * 44628 48077: contig of 3450 bp in length
 * 48078 48177: gap of 100 bp
 * 48178 52755: contig of 4578 bp in length
 * 52756 52855: gap of 100 bp
 * 52856 53293: contig of 438 bp in length
 * 53294 53393: gap of 100 bp
 * 53394 54768: contig of 1375 bp in length
 * 54769 54868: gap of 100 bp
 * 54869 57895: contig of 3027 bp in length
 * 57896 57995: gap of 100 bp

* 57996 59322: contig of 1327 bp in length
 * 59323 59422: gap of 100 bp
 * 59423 60159: contig of 737 bp in length
 * 60160 60259: gap of 100 bp
 * 60260 61231: contig of 972 bp in length
 * 61232 61331: gap of 100 bp
 * 61332 62928: contig of 1597 bp in length
 * 62929 63028: gap of 100 bp
 * 63029 63852: contig of 824 bp in length
 * 63853 63952: gap of 100 bp
 * 63953 75555: contig of 11603 bp in length
 * 75556 75655: gap of 100 bp
 * 75656 77760: contig of 2105 bp in length
 * 77761 77860: gap of 100 bp
 * 77861 79686: contig of 1826 bp in length
 * 79687 79786: gap of 100 bp
 * 79787 80857: contig of 1071 bp in length
 * 80858 80957: gap of 100 bp
 * 80958 87622: contig of 6665 bp in length
 * 87623 87722: gap of 100 bp
 * 87723 89164: contig of 1442 bp in length
 * 89165 89264: gap of 100 bp
 * 89265 90007: contig of 743 bp in length
 * 90008 90107: gap of 100 bp
 * 90108 92035: contig of 1928 bp in length
 * 92036 92135: gap of 100 bp
 * 92136 97298: contig of 5163 bp in length
 * 97299 97398: gap of 100 bp
 * 97399 102032: contig of 4634 bp in length
 * 102033 102132: gap of 100 bp
 * 102133 106605: contig of 4473 bp in length
 * 106606 106705: gap of 100 bp
 * 106706 108263: contig of 1558 bp in length
 * 108264 108363: gap of 100 bp
 * 108364 110022: contig of 1659 bp in length
 * 110023 110122: gap of 100 bp
 * 110123 113747: contig of 3625 bp in length
 * 113748 113847: gap of 100 bp
 * 113848 125151: contig of 11304 bp in length
 * 125152 125251: gap of 100 bp
 * 125252 126026: contig of 775 bp in length
 * 126027 126126: gap of 100 bp
 * 126127 129649: contig of 3523 bp in length
 * 129650 129749: gap of 100 bp
 * 129750 132160: contig of 2411 bp in length
 * 132161 132260: gap of 100 bp
 * 132261 133125: contig of 865 bp in length
 * 133126 133225: gap of 100 bp
 * 133226 135661: contig of 2436 bp in length
 * 135662 135761: gap of 100 bp
 * 135762 142148: contig of 6387 bp in length
 * 142149 142248: gap of 100 bp
 * 142249 145795: contig of 3547 bp in length.
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 * 1. 145795
 * /organism="Homo sapiens"
 * /db_xref="taxon:9606"
 * /chromosome="3"
 * /map="3p21.3"
 * /clone="RP6-91P17"
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 * ORIGIN
 * Query Match 18.9%; Score 211.4; DB 2; Length 145795;
 * Best Local Similarity 95.2%; Pred. No. 1.7e-44;
 * Matches 218; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 * QY 115 gcccttgagagaagaagagagagtggaactttgtgccgaatgcagagagagagcattc 174
 * Db 73663 GCCCTGTTTAAAGGAGAGAGTGAACCTTTGTGCCGATCCAGAGAGAGGAGCATC 73604
 * QY 175 ccccaagctgatactgaagaagatgctcatatagacaccagcgtcgcttcgtgacaag 234

|||||
Db 73603 CCCGAGGCTGTAATCTGCAAGATGCTTCATAGACACCGCTCGCTTGTGACAG 73544
QY 235 attgaagaacacctcacaaagcagagttcacttcccaagacagagcaacagcagc 294
|||||
Db 73543 ATTGAAGAGACACTCTCACAAGGACGAGTTACTTCCCAAGACAGAGCAAGGAGAC 73484
QY 295 agtcgcttctgtgtgaactctctgggagcagcagcagcagcagc 343
|||||
Db 73483 AGTCGCTTGTGTTGAACTTCTGTGGAGGACACTGACGCTGATCGAG 73435
|||||
RESULT 6
AC068720/c 202324 bp DNA HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 3 clone RP11-509121, WORKING DRAFT
DEFINITION
SEQUENCE, 20 unordered pieces.
AC068720
AC068720.2 GI:8469022
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 202324)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 202324)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 12, 2000 this sequence version replaced gi:7715661.
COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0509121
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-Primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 193150 bases at least Q40
Consensus quality: 195686 bases at least Q30
Consensus quality: 197015 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 200424; sum-of-contigs
Quality coverage: 4.67 in Q20 bases; agarose-fp
Quality coverage: 4.72 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1576: contig of 1576 bp in length
* 1577 1676: gap of unknown length
* 1677 3263: contig of 1587 bp in length
* 3264 3363: gap of unknown length
* 3364 5443: contig of 2080 bp in length
* 5444 5543: gap of unknown length
* 5544 8196: contig of 2653 bp in length
* 8197 8297: gap of unknown length
* 8297 12038: contig of 3742 bp in length

* 12039 12138: gap of unknown length
* 12139 15992: contig of 3854 bp in length
* 15993 16092: gap of unknown length
* 16093 21192: contig of 5100 bp in length
* 21193 21292: gap of unknown length
* 21293 24767: contig of 3474 bp in length
* 24767 24867: gap of unknown length
* 24867 30824: contig of 5958 bp in length
* 30825 30924: gap of unknown length
* 30925 37153: contig of 6229 bp in length
* 37154 37253: gap of unknown length
* 37254 45263: contig of 8009 bp in length
* 45263 45363: gap of unknown length
* 45363 56733: contig of 11371 bp in length
* 56734 56833: gap of unknown length
* 56834 72157: contig of 15323 bp in length
* 72157 72257: gap of unknown length
* 72257 84702: contig of 12446 bp in length
* 84703 84802: gap of unknown length
* 84803 101052: contig of 16250 bp in length
* 101053 101152: gap of unknown length
* 101153 117709: contig of 16557 bp in length
* 117710 117809: gap of unknown length
* 117810 132650: contig of 14841 bp in length
* 132651 132750: gap of unknown length
* 132751 152071: contig of 19321 bp in length
* 152072 152171: gap of unknown length
* 152172 176190: contig of 24019 bp in length
* 176191 176291: gap of unknown length
* 176291 202324: contig of 26034 bp in length.
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/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-509121"
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/note="assembly_name:Contig5"
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/note="assembly_name:Contig6"
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BASE COUNT      56787 a 45300 c 43765 g 54528 t 1944 others
ORIGIN

Query Match      18.9%; Score 211.4; DB 2; Length 202324;
Best Local Similarity 95.2%; Pred. No. 1.8e-44;
Matches 218; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 115 gccctggaagaagataaaggagggtgtgaacttctgtgcccgaatgcagaagaaggatc 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30432 GCCCTGTTTAAAGTAAAGAGAGAGTGAACCTTGTGGCCGAAATGACAGAGAGGCAATC 30373

QY 175 ccccaagctgtatactcaagaatggtctcatagacacacagcgtgctgtcttgacaag 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30372 CCCAGGCTGTATACCTGCAAGATGGCTTCATAGACACACGCCGTGGCTTCTTGACACAG 30313

QY 235 attgaaagacaactctcacaaagcagagttcacttcccaagagacagagcgaacagagc 294
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Db 30312 ATTGAAAGACACTCTCACAGAGCAGAGTTCACTCCCAAGGACAGAGCAACGAGAGC 30253

QY 295 agtgccttctgttgaacttcttgaggagcactggagcagagctccag 343
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30252 AGTGCCTTGTGTTGAACTTCTGGGGACACTGGAGCGTGAAGTCCAG 30204

RESULT 7
AC068720 AC068720 202324 bp DNA HTG 07-JUL-2000
LOCUS      Homo sapiens chromosome 3 clone RP11-509121, WORKING DRAFT
DEFINITION
SEQUENCE, 20 unordered pieces.
AC068720 AC068720.2 GI:8469022
VERSION      HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 202324)
REFERENCE      1 (bases 1 to 202324)
AUTHORS      Waterston,R.H.
JOURNAL      The sequence of Homo sapiens clone
REFERENCE      2 (bases 1 to 202324)
AUTHORS      Waterston,R.H.
JOURNAL      Direct Submission
TITLE      Submitted (07-MAY-2000) Genome Sequencing Center, Washington
          University School of Medicine, 4444 Forest Park Parkway, St. Louis,
          MO 63108, USA
COMMENT      On Jun 12, 2000 this sequence version replaced gi:7715661.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0509121
----- Summary Statistics -----
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 193150 bases at least Q40
Consensus quality: 195686 bases at least Q30
Consensus quality: 197015 bases at least Q20
Insert size: 200000; agarose-IP
Insert size: 200424; sum-of-ctrls
```

```
Quality coverage: 4.67 in Q20 bases; agarose-IP
Quality coverage: 4.72 in Q20 bases; sum-of-ctrls
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1576: contig of 1576 bp in length
1577 1676: gap of unknown length
1677 3263: contig of 1587 bp in length
3264 3363: gap of unknown length
3364 5443: contig of 2080 bp in length
5444 5543: gap of unknown length
5544 8196: contig of 2653 bp in length
8197 8296: gap of unknown length
8297 12038: contig of 3742 bp in length
12039 12138: gap of unknown length
12139 15992: contig of 3854 bp in length
15993 16092: gap of unknown length
16093 21192: contig of 5100 bp in length
21193 21292: gap of unknown length
21293 24766: contig of 3474 bp in length
24767 24866: gap of unknown length
24867 30824: contig of 5958 bp in length
30825 30924: gap of unknown length
30925 37153: contig of 6229 bp in length
37154 37253: gap of unknown length
37254 45262: contig of 8009 bp in length
45263 45362: gap of unknown length
45363 56733: contig of 11371 bp in length
56734 56833: gap of unknown length
56834 72156: contig of 15333 bp in length
72157 72256: gap of unknown length
72257 84702: contig of 12446 bp in length
84703 84802: gap of unknown length
84803 101052: contig of 16250 bp in length
101053 101152: gap of unknown length
101153 117709: contig of 16557 bp in length
117710 117810: gap of unknown length
117811 132650: contig of 14841 bp in length
132651 132750: gap of unknown length
132751 152071: contig of 19321 bp in length
152072 152171: gap of unknown length
152172 176190: contig of 24019 bp in length
176191 176290: gap of unknown length
176291 202324: contig of 26034 bp in length.

FEATURES
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    /db_xref="taxon:9606"
    /chromosome="3"
    /clone="RP11-509121"
1..1576
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1677..3263
    /note="assembly_name:Contig5"
3364..5443
    /note="assembly_name:Contig6"
5544..8196
    /note="assembly_name:Contig7"
8297..12038
    /note="assembly_name:Contig8"
12139..15992
    /note="assembly_name:Contig9
clone_end:r7
vector_side:right"
16093..21192
    /note="assembly_name:Contig10"
21293..24766
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misc_feature 45363. .56733
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misc_feature 84803. .101052
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vector_side:left"
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/note="assembly_name:Contig22"
misc_feature 176291. .202324
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BASE COUNT 56787 a 45300 c 43765 g 54528 t 1944 others
ORIGIN

Query Match 14.4% Score 161; DB 2; Length 202324;
Best Local Similarity 97.0% Pred. No. 3.2e-31;
Matches 164; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 772 aggtctagagagagctgcagagctctctctgtatataaacaagttgactactccctat 831
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Db 96876 AGGCTAGAGAGAGCTGCAGAGCTTCTCTGTATATAAACAAGTTGACCTTCCCTAT 96935
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QY 832 tccatgtcgaacctgaagaagctcactctgtctagtcga9tggagaccattgtgtgag 891
|||||
Db 96936 TCCATGCTGAGACCTGAAGAAGCTCAGCTGTAGTCGTCAGTGGGAGACCATTTGGTGAG 96995
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QY 892 ctcccaactgcctcttctgtgactatccacaccttaaatgttaagcc 940
|||||
Db 96996 CTCCCACTGCCCTTTGTGACTCATCCACCTTTAAAGTAGTAGCC 97044
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RESULT 8
LOCUS AK021919 2056 bp mRNA PRI 29-SEP-2000
DEFINITION Homo sapiens cDNA FLJ11857 fls, clone HEMBA1006807, moderately
similar to Homo sapiens mRNA for SPOB.
ACCESSION AK021919
VERSION AK021919.1 GI:10433216
KEYWORDS oligo capping; fls (full) insert sequence).
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to
mRNA, clone_11b:HEMBA1 clone:HEMBA1006807.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (sites)
REFERENCE
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K.,
Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Makanatsu,A., Nakamura,Y., Nagahari,K., Masuno,Y. and Oshima,A.
NEBO human cDNA sequencing project
TITLE Unpublished (2000)
JOURNAL 2 (bases 1 to 2056)
REFERENCE Isogai,T. and Otsuki,T.
AUTHORS Direct Submission
JOURNAL Submitted (23-AUG-2000) to the DDBJ/EMBL/Genbank databases. Takao
```

```
COMMENT
Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:genomisc@ri.co.jp,
Tel:81-438-52-3951, Fax:81-438-52-3952)
NEBO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES
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Location/Qualifiers
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VSVVQDSVNIISGHTNTWTLKVRPECLADEGLNENTRFYDCSFFVGGCFKAKSVL
AARSPVNAMEHEHMERKKNRYEINDLDEVEKEMRFYTGRAPLDGMKLANLVA
ADRYALERLKYMCSEALCSNLSEVNAVDTVLVADLHSAEDLKAQALIDFIRCSVLRL
GCKDGRKWNNSQATDIESRDRDHPFKEVKYAVIEDLKERESVPSTTTVSVSLQI"

BASE COUNT 642 a 394 c 495 g 525 t
ORIGIN

Query Match 11.7% Score 130.4; DB 9; Length 2056;
Best Local Similarity 99.2% Pred. No. 1.6e-23;
Matches 131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 985 gaataatggaagaatggaacggatcgccaacatttgataaagaagtatgaagccat 1044
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Db 1291 GACATATAGGAAGATGAAGAGGATCGCCACATTTGTGATAAGAAGTATGAAGCGCAT 1350
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QY 1045 attgaagacctaaagaagaagatctgttccagctataccaccaagtgctttagc 1104
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QY 1105 cttaacttga 1116
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Db 1411 CTTCACTTTGA 1422
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RESULT 9
LOCUS AC018500/c 150804 bp DNA PRI 19-MAR-2001
DEFINITION Homo sapiens chromosome 3 clone RP11-275J11 map 3p, complete
sequence.
ACCESSION AC018500
VERSION AC018500.3 GI:13378163
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 150804)
REFERENCE
AUTHORS Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C.,
Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
Liu,Y., Li,W., Li,W., Li,Y., Luo,C., Luo,J., Niu,Y., Qi,Q., Qi,X.,
Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H.,
Wang,J., Wang,J., Wang,L., Wang,L., Wang,L., Wang,R., Wang,X.,
Wang,X., Wang,Y., Wu,D., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X.,
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Yu.B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
Yu,J. and Yang,H.
Chromosome 3p genomic sequence
Unpublished
2 (bases 1 to 150804)
He,L., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B., Bao,W.,
Sun,Y., Wu,Q., Wang,H., Wang,X., Cheng,C., Wang,Y., Niu,Y., Qi,X.,
Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y., Li,G.,
Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,W., Li,L., Feng,X.,
Wang,X., Yu,J. and Yang,H.
Direct Submission
Submitted (13-DEC-1999) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
3 (bases 1 to 150804)
Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
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Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H.,
Wang,J., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X.,
Wang,X., Wang,Y., Wu,D., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X.,
Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
Yu,J. and Yang,H.
Direct Submission
Submitted (19-MAR-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
On Mar 19, 2001 this sequence version replaced gi:5684196.
-----Genome Center
Center: Beijing Center
Center code: Beijing
Website: http://hgci.igtp.ac.cn
http://www.genomics.org.cn
Contact: hgci@igtp.ac.cn
-----Project Information
Center project name: 18 project
Center clone name: RP11-275J11
-----Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 152846 bases at least Q40
Consensus quality: 153558 bases at least Q30
Consensus quality: 153695 bases at least Q20
Insert size: 150804; sum-of-contigs
Quality coverage: 10.96x in Q20 bases; sum-of-contigs
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/clone="RP11-275J11"
BASE COUNT 40688 a 33310 c 33710 g 43096 t
ORIGIN
Query Match 7.2%; Score 80.2; DB 9; Length 150804;
Best Local Similarity 73.0%; Pred. No. 5.4e-10;
Matches 103; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 137 aggggaacttggcgcatgacggagggagggcattcccccaagcgtatctacgaaga 196
DB 28318 AATTAACCTATTATTAATAAATTCAGAGTAAGACATTCCTCCAGCATGCTGCAGAGA 28259
QY 197 atggttcataagacaccagcgtggcgtctctgcacaagattgaagaagaacactctcaaa 256

```


Yu, J. and Yang, H.
Direct Submission
Submitted (20-MAR-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing,
100101, P.R. China
On Mar 20, 2001 this sequence version replaced gi:8072552.

On Mar 20, 2001 this sequence version replaced gl:8072582.
-----Genome Center

Center: Beijing Center
Center code: Beijing
Website: <http://hgsc.igtp.ac.cn>
<http://www.genomics.org.cn>
Contact: hgsc@igtp.ac.cn
----- Project Information -----
Center project name: 1% project
Center clone name: RP11-30623

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----- Summary Statistics -----
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; Er 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; Version 0.990329
Consensus quality: 499 bases at least Q40
Consensus quality: 605 bases at least Q30
Consensus quality: 674 bases at least Q20
Insert size: 692; sum-of-contigs
Quality coverage: 2.80x in Q20 bases;sum-of-c-
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Location/Qualifiers
1. .166043

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"

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/clone="RP11-30G23"
BASE COUNT 48570 a 35113 c 34446 g 47914 t
ORIGIN

```

7.2%; Score 80.2; DB 9; Length 166043;

Best Local Similarity 73.0%; Pred. NO. 5.4e-10;
Matches 103; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Oy 137 agtggacctttgtgcccgaatgcagcaggagaagygcatcccccaagctgttactcycaaga 196
| | | | | | | | | | | | | | | | | | | |
Db 10231 AATAACCTATTTTAAAAAATTGAGAGTAAGAACAATTCCCGAGGCATGTCCTCAGA 10290

Qy 197 atggtctcatagacaccgcgtgcgtcttcttgacaagaatltgaagaaacctctcaaa 256
||| ||||| ||| ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10291 ATGACTTCACAGATACCAGCGCTGAAGCTTCTAGAAAAGATAGAAGAAACCCCTCAGGAA 103

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QY      257  ggcagagttcacttcccaag  277
          || ||| ||||| |||
Db 10351  GGTAGAGCTCACTTCCCAGG 10371
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LOCUS	185608 bp	DNA	PRI	06-MAR-2007
AC027126				
DEFINITION	Homo sapiens chromosome 3 clone RP11-586C12 map 3p, complete			

AC027126.4 GI:13236635

human.

REFERENCE
AUTHORS

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 185608)
Wu, Q., Bao, T., Bao, Q., Cao, W., Bian, X., Cao, T., Chen, C., Chen, J.,

1. (bases 1 to 185608)
 Wu, Q., Bao, Y., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J.,
 Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guo, Q., Gu, X., Guo, D.,
 Guo, Z., He, L., Hu, S., Huang, P., Jin, Y., Kang, N., Li, C., Li, C.,
 Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B.,
 Liu, Y., Li, W., Li, W., Li, Y., Luo, C., Luo, J., Niu, Y., Qi, Q., Qi, K.,
 Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H.,

Wang, J., Wang, J., Wang, J., Wang, L., Wang, R., Wang, X., Wang, X., Wang, X., Wu, D., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X. Y., B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J., and Yang, H.

Chromosome 3p genomic sequence

Unpublished

2 (bases 1 to 185608),
Tao, R., Hu, S., Dong, W.

Direct Submission
Submitted (28-MAR-2000) Human Genomic Center, Institute of

3 (bases 1 to 185608)
Wu,Q., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,

Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, F., Luo, C., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J., and Yang, H.

Direct Submission
Submitted (06-MAR-2001) Human Genomic Center, Institute of
Genetics, University of California, Davis, CA 95616, USA

On Mar 6, 2001 this sequence version replaced gi:8101246.
-----Genome Center.

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Center:Beijing Center
Center code:Beijing
Website:http://hgc.igbp.ac.cn
http://www.genomics.org.cn
Contact:hgc@igbp.ac.cn

----- Project Information
Center project name:18 project
Center clone name: RP11-586C12

----- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; ET 5% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 187858 bases at least Q40
Consensus quality: 189056 bases at least Q30
Consensus quality: 189280 bases at least Q20
Insert size: 185608; sum-of-contigs
Quality coverage: 10..96x in Q20 bases;sum-of-contigs

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Location/Qualifiers
1. .185608

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"

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ORIGIN								

Sequence	Score	DB	Length
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1 Similarity	73.08;	Pred. No. 5.6e-10;	
103; Conservative	0;	Mismatches 38;	Indels 0;
			Gaps 0;

Oy 137 agtggaaactttgtgcccgaatgcaggaagaaggcatccccacgctgttacctcaaga 196
| | | | | | | | | | | | | | | | | | | | |
Db 54490 AATAAAGCATTTTAAAAAATTTCAGAAGTAAGACATTCGCCAGCCATGTCTGCAAGA 54549

OY 728 atalcagcaataaccctgaccgacgtgcgaagatatagacagctagagagctgc 787
 Db 148553 GTTTTATGGAATTAATTATTCGAAATCCCTGTGGACATGCTTCAGTACGACGCTGC 148494
 OY 788 agagcttctctgtataaacaagctgacctacccttc 827
 Db 148493 TTCATTAGAGTTGAATAGAAACAACACTCACCGTATTTTC 148454

RESULT 14
 AC092762
 LOCUS AC092762
 DEFINITION Pan troglodytes clone RP43-10804, WORKING DRAFT SEQUENCE, 9
 unorderd pieces.
 AC092762 169580 bp DNA 26-JUL-2001
 AC092762.1 GI:15022031
 VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS chimpanzee.
 SOURCE Pan troglodytes
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 REFERENCE 1 (bases 1 to 169580)
 Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E., Lee, L.S.-Q., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Masello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Zhang, L.-H. and Green, E.D.
 NISC Comparative Sequencing Initiative
 Unpublished
 2 (bases 1 to 169580)
 Green, E.D.
 DIRECT SUBMISSION
 Submitted (26-JUL-2001) NIH Intramural Sequencing Center, 8717
 Grovmont Circle, Gailthersburg, MD 20877, USA
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC
 Web site: http://www.nisc.nih.gov
 Contact: nisc-mousehgri.nih.gov
 ----- Project Information
 Center project name: ano
 Center clone name: 108004
 ----- Summary Statistics
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 164694 bases at least Q40
 Consensus quality: 165758 bases at least Q30
 Consensus quality: 166599 bases at least Q20
 Insert size: 14100; agarose-fp
 Insert size: 13200; pulse-field-gel
 Insert size: 168780; sum-of-contigs
 Quality coverage: 14.4ix in Q20 bases; agarose-fp
 Quality coverage: 15.4ix in Q20 bases; pulse-field-gel
 Quality coverage: 12.04x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 2898: contig of 2898 bp in length
 * 2899 2898: gap of unknown length
 * 2899 9905: contig of 6907 bp in length
 * 9906 10005: gap of unknown length
 * 10006 16835: contig of 6830 bp in length

16836 16935: gap of unknown length
 * 16936 24424: contig of 7489 bp in length
 * 24425 24524: gap of unknown length
 * 24525 38758: contig of 14234 bp in length
 * 38759 38858: gap of unknown length
 * 38859 53065: contig of 14207 bp in length
 * 53066 53166: gap of unknown length
 * 53166 74767: contig of 21601 bp in length
 * 74767 74867: gap of unknown length
 * 74867 96507: contig of 21640 bp in length
 * 96507 96607: gap of unknown length
 * 96607 169580: contig of 72974 bp in length.
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 /db_xref="taxon:9596"
 /clone="RP43-10804"
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 1. 2898
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 10006. 16835
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 16936. 24424
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 24525. 38758
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 clone_end:T7
 vector_side:left
 38859. 53065
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 53166. 74766
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 96607. 169580
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Query Match 5.8%; Score 64.4; DB 2; Length 169580;
 Best Local Similarity 48.8%; Pred. No. 7.8e-06;
 Matches 204; Conservative 0; Mismatches 211; Indels 3; Gaps 1;

OY 407 ttccatataatcagttatttcaagcgtatgaattctgagctgcacaaaccaa 466
 Db 158446 TTCCATCTGAATTAATTCATTACTTACTTAATTAAGATTAATTAAGTCAATACACACA 158505
 OY 467 ttccatcttcagcagaatcgtgttttgaagaacctgaagaacctgaatgtgtgt 526
 Db 158506 TATCACAATATACCTTAAGAAATATATCATGCTTGGAATATACACACACTCTTTTATATA 158565
 OY 527 tcaactctcgaagagcattccctcagaatgttgagagatttgaagaacctgagagactgtg 586
 Db 158566 ACAATTACATTTGAATAATTTCTTACCTGACCTAGTAATCTTGGAACTTGA--AAFTT 158622
 OY 587 attgtctggaatctagaattatgagctgcaccttgattgaatgaattgaagaag 646
 Db 158623 TAACTTTGGGTAATAAATTAAGTAAAGATATATACAGTACTCTGCTTAATTAATAACT 158682
 OY 647 ttcaattttagatataatcagcaagaagtttccagtgctcccaatctgtctcgcgga 706
 Db 158683 TGAGGCTTCTCAATTTGGAATATATATGATTAACAATATTTCTTAAGCTCTGCTTCC 158742
 OY 707 tgtcgaatttgcagtggtgtgatatcagcagcaataaccctgagcagctcgcgcaagata 766
 Db 158743 TTCCAAGATTAATTTTCACTGACCTTACTGGAACCTTAATTAAGCAGTTTCCAAAGAAA 158802
 OY 767 tagacaagctagagagctgagagcttctctgtataaacaagttgacctact 824

Db 158803 TTAGGACCTTTAAATTTAGAAACACTTTTATGATCACAATATGCTTACCTTCTT 158860

RESULT 15
AF359380 1658 bp mRNA PRI 12-JUL-2001
LOCUS Homo sapiens LANO adaptor protein (LANO) mRNA, complete cds.
DEFINITION AF359380
ACCESSION AF359380.1 GI:14701833
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1658)
Saito, H., Santoni, M.-J., Jaulin-Bastard, F., Marchetto, S.,
Isardon, D., Adelaide, J., Birnbaum, D. and Borg, J.-P.
TITLE Lano, a novel LAP protein directly connected to MAGUK proteins in
epithelial cells
JOURNAL J. Biol. Chem. (2001) In press
REFERENCE 2 (bases 1 to 1658)
Saito, H., Marchetto, S., Birnbaum, D. and Borg, J.-P.
AUTHORS Direct Submission
JOURNAL Submitted (12-MAR-2001) Molecular Oncology, U119 INSERM, 27,
Boulevard Lei Roure, Marseille 13009, France
FEATURES
source Location/Qualifiers
1..1658
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..1658
/gene="LANO"
1..1575
/gene="LANO"
/note="belongs to the LAP protein family with mammalian
Erbin, Scribble and Densin-180 but contains no PDZ domain;
interacts with MAGUKs (DLG) and LAP proteins (Erbin);
contains LRR motifs, a LAP specific domain (LAPSD), and a
C-terminal MAGUK PDZ domain binding site"
/codon_start=1
/product="LANO adaptor protein"
/protein_id="AAK72246.1"
/db_xref="GI:14701834"
/translation="MFHCITPLMRCNHRVESIDKRHCSLYVPEITRYARSLEBLID
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FCALOVADPSGNPLRLPESFELQNTCSYNDISQSLPENIGNMYNLASLEIRE
NLITYLPDSLTLRLLELDLGNNEIYNLDESIGALLHLKMDLMDGNQSLSELPOEIGN
LKNLLCLDVSNNRLERLPEEISGLTSLDLVISQNLLETIPDGKGLKRTSLKVDGN
RLTQLEPAVGECSLPELVLTENQLTLPKSGIKKLSNMDNRKLVSLPRKIGSC
CSITVECRNRLRTRIPAVSQATELHVLVDVAGNRLHPLSLTALKLKLMDLSDNS
QPLTRQTDYDTTGEKILTCVLPLPQSPSEPTCOENLPCGALENLVNDVSDENMR
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NKNENVNHAIIDRVTTTSV"

BASE COUNT 483 a 383 c 378 g 414 t
ORIGIN

Query Match 5.7%; Score 63.6; DB 9; Length 1658;
Best Local Similarity 46.4%; Pred. No. 5.7e-06;
Matches 244; Conservative 0; Mismatches 279; Indels 3; Gaps 1;

QY 383 taagcaataccttgatcaatcaatccttctacatataatcagttatccaagcgatgagaa 442
DB 404 TAAATGACATCTACTACTCTTACCTGAAATATTGGCAATCTTATTAACCTGGCTT 463
QY 443 ttctgatactgcgaataaacaatcacaatccttcagcagaaatcggtgttgaaga 502
DB 464 CACTGGAACTGAGAGAAATCTTCTTACATATCTTCCGACTCTCTTAACCAAGCTGGCAA 523
QY 503 acctgaagaactcaatctgtgttcaactatctgaagagcattccctccagaattggag 562
DB 524 GACTAGAGAACTGATTAGGAAACAATGAAATATATATTTCAGCAATCAATTTGGAG 583

QY 563 atttgaaaatctagagagactggaattgttctggaatctagaatataatgagctgcct 622
DB 584 CCCTCTTACATCTTAAAGATCTCTGTGGATGGAAATCAACTGTCA--GAAATACCTC 640
QY 623 ttgaataagtaattggaagcaagttacattgtatagataatccagcaacaagtttcca 682
DB 641 AGGAATATAGAAATCTGAAAGAACCTGCTGTGTTTATGATGTCTCTTAAACAGAGTGGAAA 700
QY 683 gtgcccacatctgtgctcgtcggaatgtcgaattgtcagtggttgatatacagcaagaata 742
DB 701 GACTTCTGAGAAATCAAGTGGCTGCTGACTTCAATTAACGGATTACTCAATTCAGAACT 760
QY 743 acctgacccgacctgcgcgaagatatagacagcctagagagctgacagcttctcttct 802
DB 761 TATTGAAACGATTCGCGATGGCATTGGAAACCTAAAGAACTGTGAAGGTGG 820
QY 803 ataaacaagtgtagcctacccttccctatccatgctgaacctgagaagcctcactctgt 862
DB 821 ATCAGAAATAGACTCACACAGTTGCTTGAAGCAGTTGGGGAATGTGAAGTCTCACTGAGT 880
QY 863 tagtcgtagtgggagaccatttggtgagagctcccaactgccttgg 908
DB 881 TAGTCTTACAGAAATCAGCTCCTGACCCCTGAAAGCATTTGG 926

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